Bre1p-mediated histone H2B ubiquitylation regulates apoptosis in Saccharomyces cerevisiae

David Walter, Anja Matter and Birthe Fahrenkrog

M. E. Müller Institute for Structural Biology, Biozentrum, University of Basel, CH-4056 Basel, Switzerland

*Present address: Institute for Molecular Biology and Medicine, Université Libre de Bruxelles, 6041 Gosselies, Belgium

†Author for correspondence (bfahrenk@ulb.ac.be)

Accepted 22 March 2010
Journal of Cell Science 123, 1931-1939
© 2010. Published by The Company of Biologists Ltd
doi:10.1242/jcs.065938

Summary

BRE1 encodes an E3 ubiquitin protein ligase that is required for the ubiquitylation of histone H2B at lysine 123 (K123). Ubiquitylation of this histone residue is involved in a variety of cellular processes including gene activation and gene silencing. Abolishing histone H2B ubiquitylation also confers X-ray sensitivity and abrogates checkpoint activation after DNA damage. Here we show that Saccharomyces cerevisiae Bre1p exhibits anti-apoptotic activity in yeast and that this is linked to histone H2B ubiquitylation. We found that enhanced levels of Bre1p protect from hydrogen-peroxide-induced cell death, whereas deletion of BRE1 enhances cell death. Moreover, cells lacking Bre1p show reduced lifespan during chronological ageing, a physiological apoptotic condition in yeast. Importantly, the resistance against apoptosis is conferred by histone H2B ubiquitylation mediated by the E3 ligase activity of Bre1p. Furthermore, we found that the death of Δbre1 cells depends on the yeast caspase Yca1p, because Δbre1 cells exhibit increased caspase activity when compared with wild-type cells, and deletion of YCA1 leads to reduced apoptosis sensitivity of cells lacking Bre1p.

Key words: Apoptosis, Histone H2B, S. cerevisiae, Ubiquitin, YCA1

Introduction

Apoptosis is a form of programmed cell death that has a central role in development and cellular homeostasis in higher eukaryotes. Knowledge of apoptotic regulation is particularly important for medical research, since apoptotic misregulation is implicated in many human diseases, such as Alzheimer’s disease and Huntington’s disease, immunodeficiency and cancer (Fadeel and Orrenius, 2005). Recent studies have established yeast as a model to study the mechanisms of apoptotic regulation. Defects in distinct cellular processes, such as actin dynamics (Gourlay et al., 2004), vesicular fusion (Madoe et al., 1997), DNA replication (Weinberger et al., 2005), histone chaperone activity (Yamaki et al., 2001) or histone deubiquitylation (Bettiga et al., 2004) can trigger apoptotic cell death in Saccharomyces cerevisiae and an apoptotic-like phenotype has also been demonstrated in yeast cells treated with various agents including hydrogen peroxide, acetic acid and pheromone (Ludovico et al., 2001; Madoe et al., 1999; Severin and Hyman, 2002). Notably, the yeast apoptotic machinery has functional orthologues of key mammalian apoptotic regulators, including the metacaspase Yca1p (Madoe et al., 2002), the apoptosis-inducing factor AIF (Wissing et al., 2004), the endonuclease EndoG (Bettiga et al., 2004), the serine protease HtrA2/Omi (Fahrenkrog et al., 2004) and the inhibitor-of-apoptosis protein Bir1p (Walter et al., 2006). In addition, yeast apoptosis has been linked to cellular events such as mitochondrial fragmentation (Fannjiang et al., 2004), cytochrome c release (Ludovico et al., 2002), ageing (Herker et al., 2004; Laun et al., 2001) and phosphorylation of histone H2B (Ahn et al., 2005; Ahn et al., 2006).

Rapid protein modifications allow the cell to promptly adapt to environmental changes by different cellular responses, including apoptosis. The post-translational modification by covalent attachment of ubiquitin is one of the major biochemical mechanisms that regulate apoptosis (Lee and Peter, 2003). Ubiquitylation controls the level of proteins by targeting them for proteasomal degradation. Members of the inhibitor-of-apoptosis protein (IAP) family are targeted for degradation, but they also contain a RING domain with ubiquitylating activity, by which they are able to mark other proteins such as caspases for degradation (Wilson et al., 2002). Additionally, monoubiquitylation and nonclassical polyubiquitylation of components of the apoptotic pathway regulate apoptosis on a molecular level, beyond the degradation effects (Huang et al., 2000; Lee et al., 2002; Mimnaugh et al., 2001).

Histone proteins are well-known substrates for numerous covalent post-translational modifications and these modifications regulate a number of cellular processes including apoptosis (Ahn et al., 2005; Ahn et al., 2006; Cheung et al., 2003). Histone H2B is monoubiquitylated at Lys123 by the ubiquitin conjugase Rad6p and the E3 ligase Bre1p (Hwang et al., 2003; Robzyk et al., 2000; Wood et al., 2003b). BRE1 disruption or lysine-to-arginine substitution at residue 123 of histone H2B (H2B-K123R), results in a complex phenotype that includes failures in gene activation (Henry et al., 2003; Kao et al., 2004; Wyce et al., 2007; Xiao et al., 2005) and lack of telomeric silencing (Briggs et al., 2001; Dover et al., 2002; Mutiu et al., 2007; Sun and Allis, 2002). Moreover, Caenorhabditis elegans BRE1 was identified in a screen for anti-apoptotic proteins (Lettre et al., 2004). Only recently, histone H2B ubiquitylation has been implicated in DNA repair and checkpoint activation after DNA damage (Game et al., 2006; Giannattasio et al., 2005). As the DNA damage response machinery is closely linked to apoptosis in yeast and higher eukaryotes (Burhans et al., 2003) a relationship between histone H2B ubiquitylation and apoptosis might exist. This possibility is supported by the finding that loss of the ubiquitin-specific protease UBP10, which is involved in cleaving the ubiquitin moiety from
histone H2B, causes caspase activation and apoptosis in yeast (Bettiga et al., 2004).

We aimed to gain insight into the role of histone H2B ubiquitylation in apoptosis and found that *S. cerevisiae* Bre1p exhibits anti-apoptotic activity in yeast and that this is linked to histone H2B ubiquitylation and the metacaspase Yca1p.

**Results**

Bre1p protects against hydrogen-peroxide-induced cell death in budding yeast

The E3 ubiquitin ligase Bre1p is required for histone H2B ubiquitylation (Hwang et al., 2003; Robzyk et al., 2000; Wood et al., 2003b), which in turn is implicated in transcriptional regulation and DNA repair. Moreover, H2B ubiquitylation appears to have a role in apoptosis regulation because the loss of the ubiquitin-specific protease UBP10, which is involved in cleaving the ubiquitin moiety from histone H2B, causes caspase activation and apoptosis in yeast (Bettiga et al., 2004). Notably, the *C. elegans* homologue of the *S. cerevisiae* Bre1p was identified as a regulator of germ-cell apoptosis in worms (Lettre et al., 2004), further supporting the importance of H2B ubiquitylation in apoptosis regulation.

To explore a role for Bre1p-mediated histone H2B ubiquitylation in yeast apoptosis, wild-type cells, cells lacking *BRE1* (*H9004 bre1*) and cells constitutively overexpressing a protein-A-tagged Bre1p fusion protein (ProtA-Bre1p) under the control of the *NOP1* promoter were exposed to 0.6 mM hydrogen peroxide (H2O2) to induce apoptosis. After 8 hours of incubation, cell survival was determined by clonogenicity and cells were tested for apoptotic markers, such as DNA single-strand breaks and reactive oxygen species (ROS), which are causally linked to yeast apoptosis. To do so, cells were stained with dihydroethidium (DHE) to visualise accumulation of ROS and TUNEL labelling was used to detect single-stranded DNA breaks. As shown in Fig. 1A, yeast cells lacking *BRE1* exhibited an increased sensitivity to H2O2 (31±4% cell viability) compared with wild-type (wt) cells (53±6% cell viability). This increase in sensitivity to H2O2 of Δ*bre1* cells was accompanied by enhanced ROS production (54±4% of Δ*bre1* versus 25±2% of wild-type cells were DHE positive; Fig. 1B,C) and by an increase in apoptotic DNA fragmentation and TUNEL-positive cells compared with wild-type cells (25±3% versus 14±1% TUNEL-positive cells; Fig. 1B,D). By contrast, cells overexpressing ProtA-Bre1p showed resistance to H2O2 (78±7% cell viability; Fig. 1A) and a decrease in ROS accumulation (15±1% DHE-positive cells; Fig. 1B,C) and DNA fragmentation (5±1% TUNEL-positive cells; Fig. 1B,D). Taken together, our data indicate that Bre1p exhibits anti-apoptotic activity.

Disruption of *BRE1* causes an early onset of cell death during chronological ageing

Chronological ageing defines an ageing process of post-mitotic yeast cells that triggers apoptosis (Herker et al., 2004). Therefore, we next investigated whether or not Bre1p is involved in chronological ageing. To do so, we determined the chronological lifespan of cells lacking *BRE1* and found that these cells showed an early onset of age-induced cell death when compared with wild-type cells (Fig. 2A). After 2 days in culture, cells lacking *BRE1* showed survival rates of 23±4% compared with 75±5% in wild-type cells (Fig. 2A). When, after 2 days in culture, these yeast cells were tested for apoptotic markers, Δ*bre1* cells showed typical hallmarks of apoptosis, such as the production of ROS as detected by DHE staining (77±3% of Δ*bre1* versus 16±4% of wild-type cells were DHE positive; Fig. 2B,C) and an increase in apoptotic DNA fragmentation as detected by TUNEL labelling (26±4% of Δ*bre1* versus 6±1% of wild-type cells were TUNEL positive; Fig. 1932 Journal of Cell Science 123 (11)
The E3 ligase activity of Bre1p is required for its anti-apoptotic properties

A hallmark of Bre1p is a C-terminal C3HC4 (RING) zinc-finger domain (Hwang et al., 2003). RING domains are typically found in E3 ubiquitin ligases and frequently mediate the interaction with the E2 ubiquitin-activating enzyme (Deshaies and Joazeiro, 2009). The RING domains are therefore crucial for catalysing the transfer of ubiquitin from the E2 to the substrate. Accordingly, the RING domain of Bre1p confers E3 ubiquitin ligase activity, which is required for the ubiquitylation of histone H2B (Hwang et al., 2003; Wood et al., 2003a). To test whether the E3 ligase activity is required to grant resistance to age-induced apoptosis, we generated two different RING-domain mutants. First, two conserved cysteine residues (C648 and C651) within the RING domain were mutated to glycine and second, leucine L650 was mutated to glutamate (L650E). Although the mutation of the cysteines might affect the overall folding of the RING domain, L650 probably mediates the interaction of Bre1p with its E2 ligase, but does not affect the zinc coordination and stability of the protein. We next complemented Δbre1 and Δbre1 cells expressing H2B-GFP (Δbre1 HTB1-GFP), respectively, with plasmid-borne ProtA-Bre1p, ProtA-Bre1p(C648G, C651G) and ProtA-Bre1p(L650E) and tested the functionality of the ProtA-Bre1p, ProtA-Bre1p(C648G, C651G) and ProtA-Bre1p(L650E) as a measure of their ability to ubiquitylate histone H2B.

Monoubiquitylation of histone H2B can be detected in wild-type cells harbouring a functional GFP-tagged allele of the HTB1 gene (encoding histone H2B) as a slower-migrating form upon SDS-PAGE and immunoblotting of whole-cell extracts with anti-GFP antibody. The ubiquitylated species was absent in Δbre1 cells harbouring a GFP-tagged allele of HTB1 (Fig. 3A), which is consistent with a previous study (Wood et al., 2003a). However, Δbre1 HTB1-GFP cells complemented with ProtA-Bre1p displayed no defect in H2B monoubiquitylation, whereas Δbre1 HTB1-GFP cells complemented with ProtA-Bre1p(C648G, C651G) and ProtA-Bre1p(L650E), respectively, lacked ubiquitylation of histone H2B similarly to Δbre1 HTB1-GFP cells (Fig. 3A). We conclude that the ProtA-Bre1p fusion protein is functional and that Bre1p requires the conserved cysteines C648, C651 and leucine 650 for its E3 ligase activity.

To explore the contribution of the E3 ligase activity of Bre1p to apoptosis resistance, we analysed the survival of Δbre1 cells complemented with ProtA-Bre1p, ProtA-Bre1p(C648G, C651G) and ProtA-Bre1p(L650E) during chronological ageing. BRE1-null cells complemented with ProtA-Bre1p showed no significant difference in cell survival when compared with wild-type cells (89±5% cell viability versus 92±5% cell viability after 2 days in culture; Fig. 3A). Consistently, Δbre1 cells complemented with ProtA-Bre1p and wild-type cells showed similar amounts of apoptotic markers with ~16% DHE-positive cells and 6-7% TUNEL-positive cells, respectively (Fig. 3D-F). By contrast, Δbre1 cells complemented with ProtA-Bre1p(C648G, C651G) or ProtA-Bre1p(L650E) showed an early onset of cell death during chronological ageing similarly to Δbre1 cells (21±2% and 23±1% cell viability versus 23±4% cell viability after 2 days in culture; Fig. 3B). 79±6% of Δbre1 cells complemented with Bre1p(C648G, C651G) showed ROS accumulation and 25±3% were TUNEL positive, similarly to Δbre1 cells (77±3% ROS-positive, 26±4% TUNEL-positive cells; Fig. 3D-F).

Consistent with the chronological ageing experiments, plasmid-borne ProtA-Bre1p, but not ProtA-Bre1p(C648G, C651G) or ProtA-Bre1p(L650E) rescued Δbre1 cells from H2O2-induced cell death (Fig. 3C). H2O2-treated cells lacking BRE1 that were complemented with ProtA-Bre1p showed a slightly better cell survival than wild-type cells (67±5% cell viability versus 54±6% cell viability; Fig. 3C) and fewer apoptotic markers (18±5% versus 25±2% DHE-positive cells as well as 8±3% versus 14±1% TUNEL-positive cells; Fig. 3D,G,H). However, Δbre1 cells complemented with ProtA-Bre1p(C648G, C651G) or ProtA-Bre1p(L650E) showed H2O2 sensitivity that was similar to Δbre1 cells (35±2% and 33±3% cell viability versus 31±4% cell viability; Fig. 3C). 48±3% of Δbre1 cells complemented with Bre1p(C648G, C651G) showed ROS accumulation and 26±2% were TUNEL positive, similarly to Δbre1 cells (54±4% ROS positive, 25±3% TUNEL positive; Fig. 3D,G,H). We conclude that the E3 ligase activity of Bre1p is required for its ability to confer resistance to apoptosis.

Bre1p confers apoptosis resistance by histone H2B ubiquitylation

Bre1p targets Lys123 in histone H2B for ubiquitylation. We therefore asked whether the ubiquitylation site of histone H2B is
required for the anti-apoptotic property of Bre1p. To address this question, we analysed the chronological lifespan of the yeast strain 
\textit{FLAG-htb1K123R}, which expresses a FLAG-tagged histone H2B variant containing a lysine-to-arginine substitution at Lys123 and therefore fails to be ubiquitylated (Sun and Allis, 2002). We found that these cells showed an early onset of cell death during chronological ageing, similarly to \textit{bre1} \textit{FLAG-HTB1} cells that lack \textit{BRE1} and express FLAG-tagged wild type histone H2B (36±7% cell viability versus 32±5% cell viability after 3 days in culture; Fig. 4A).

We next determined whether the lack of Bre1p and the lack of histone H2B ubiquitylation affect the same pathway leading to an early onset of cell death during chronological ageing. To do so, we disrupted \textit{BRE1} in \textit{FLAG-htb1K123R} cells and analysed the chronological lifespan of the resulting double mutant \textit{Δbre1 \textit{FLAG-htb1K123R}}. An additive phenotype for the double mutant is expected if the two mutations affect the chronological lifespan of yeast independently. However, the double mutant strain \textit{Δbre1 \textit{FLAG-htb1K123R}} showed no further decrease in survival during chronological ageing when compared with either single mutant (35±5% cell viability versus 36±7% and 32±5% cell viability, respectively, after 3 days in culture; Fig. 4A), indicating that both mutations affect the same pathway. Moreover, these data suggest that Bre1p confers resistance to age-induced apoptosis by mediating histone H2B ubiquitylation. Likewise, \textit{FLAG-htb1-K123R} mutant cells showed H2O2 sensitivity that was similar to that in \textit{Δbre1 \textit{FLAG-HTB1}} cells (66±7% cell viability versus 69±7% cell viability; Fig. 4B), whereas the double mutant strain \textit{Δbre1 \textit{FLAG-htb1K123R}} exhibited no further decrease in survival when compared with either single mutant (70±6% cell viability versus 66±7% and 68±7% cell viability, respectively; Fig. 4B). Together, our data indicate that Bre1p
diminishes apoptotic death by mediating histone H2B ubiquitylation.

**Death of ∆bre1 cells depends on the yeast metacaspase Yca1p**

Yeast cells lacking BRE1 were sensitive to apoptotic stimuli and displayed morphological markers of apoptosis upon H2O2 treatment and during chronological ageing (Figs 1 and 2). Apoptosis in yeast can occur in a caspase-dependent or caspase-independent manner (Madeo et al., 2009). To investigate whether the yeast metacaspase Yca1p is involved in the death of ∆bre1 cells, we generated a ∆yca1∆bre1 double-mutant strain. The death rate during chronological ageing was decreased in ∆bre1 cells compared with ∆bre1 cells (47±3% cell viability versus 21±2% cell viability after 2 days in culture; Fig. 5A), indicating that Yca1p is required for cell death of ∆bre1 cells. However, the death of ∆bre1 cells is not exclusively Yca1p-dependent during chronological ageing as the double mutant ∆bre1∆yca1 exhibited a higher death rate than wild type cells (47±3% cell viability versus 75±5% cell viability after 2 days in culture; Fig. 5A). In addition, ∆bre1∆yca1 cells displayed less ROS accumulation during chronological ageing when compared with ∆bre1 cells (41±4% versus 77±3% cells were DHE positive after 2 days in culture; Fig. 5B), but more than wild-type cells (41±4% versus 15±3% cells were DHE positive after 2 days in culture; Fig. 5B). Therefore, the death of ∆bre1 cells during chronological ageing is partially Yca1p dependent. Notably, unlike ∆bre1 cells, ∆bre1∆yca1 cells did not display apoptotic DNA fragmentation during chronological ageing as detected by TUNEL labelling (supplementary material Fig. S1), suggesting that ∆bre1∆yca1 cells die in a necrotic rather than apoptotic fashion. Annexin-V and propidium iodide (PI) costaining was used to further analyse apoptotic externalisation of phosphatidylserine and necrotic membrane permeabilisation. ∆bre1 cells, unlike ∆bre1∆yca1 cells, displayed externalisation of phosphatidylserine as detected by annexin-V staining (supplementary material Fig. S1), further supporting the notion that ∆bre1 cells die in an apoptotic manner, whereas the death of ∆bre1∆yca1 cells is of a necrotic nature.

Next, we tested the response of ∆bre1∆yca1 cells to H2O2 exposure. As shown in Fig. 5C, the death rate after H2O2 treatment was decreased in ∆bre1∆yca1 cells when compared with ∆bre1 cells (57±5% cell viability versus 32±5% cell viability; Fig. 5C). Unlike during chronological ageing, the death of ∆bre1 cells seems to be exclusively Yca1p dependent after H2O2 treatment, because the double-mutant ∆bre1∆yca1 cells show survival rates similar to wild-type cells (57±5% cell viability versus 50±6% cell viability; Fig. 5C). In addition, the population of ∆bre1∆yca1 cells with ROS accumulation after H2O2 treatment was smaller when compared with ∆bre1 cells but similar to wild-type cells (23±1% DHE-positive ∆bre1∆yca1 cells compared with 53±7% DHE-positive ∆bre1 and 23±3% DHE-positive wild type cells; Fig. 5D). Taken together, our data indicate that Yca1p is required to activate apoptosis in ∆bre1 cells in response to H2O2 treatment.

Apoptosis in yeast can also be Yca1p independent. The mitochondria-localised apoptosis-inducing factor Aif1p (Wissing
Cells lacking BRE1 show increased caspase activity

Since disruption of YCA1 desensitises Δbre1 cells towards apoptotic stimuli, we asked whether or not the caspase activity of Yca1p is involved in cell death execution of Δbre1 cells. To address this question, we tested whether Δbre1 cells exhibited higher caspase activity after induction of apoptosis compared with wild-type cells. To monitor potential caspase activation, yeast cells were incubated with FITC-labelled VAD-fmk (FITC-VAD-fmk). FITC-VAD-fmk binds specifically to the active centre of metazoan caspases, which enables a flow-cytometric determination of caspase activity.

Fig. 6. Cells lacking BRE1 show increased caspase activity. (A) Chronological aged wild-type and Δbre1 cells and cells treated with 0.6 mM H2O2 were labelled with FITC-VAD-fmk and propidium iodide (PI) and analysed by flow cytometry. One representative experiment from three independent experiments with similar results is shown. (B) Chronological aged wild-type and Δbre1 cells and cells treated with 0.6 mM H2O2 were incubated with the caspase substrate (L-Asp)2 rhodamine 110 (D2R) and analysed by flow cytometry. One representative experiment from three independent experiments with similar results is shown.

Discussion

BRE1 encodes an evolutionarily conserved E3 ubiquitin ligase that, in yeast, catalyses monoubiquitylation of histone H2B at lysine 123 (K123). Histone H2B K123 ubiquitylation is involved in a variety of cellular processes, such as gene activation, gene silencing and checkpoint activation after DNA damage (Briggs et al., 2001; Dover et al., 2002; Game et al., 2006; Giannattasio et al., 2005; Henry et al., 2003; Kao et al., 2004; Mutiu et al., 2007; Sun and Allis, 2002; Wyce et al., 2007; Xiao et al., 2005). Here, we uncover a new role for Bre1p and show that S. cerevisiae Bre1p protects yeast cells from H2O2-induced cell death, whereas deletion of BRE1 enhances cell death and leads to decreased lifespan during chronological ageing. Also, we show that Bre1p activity in yeast apoptosis requires its E3 ubiquitin ligase activity, thereby linking yeast apoptosis to histone H2B monoubiquitylation. Furthermore, we show that Bre1p protects yeast cells from death in a Yca1p-dependent manner.

A role for Bre1p in programmed cell death

Enhanced levels of Bre1p protect yeast from H2O2-induced cell death and diminish the development of apoptotic hallmarks, such as ROS accumulation and DNA single-strand breaks (Fig. 1). By contrast, cells lacking Bre1p are more sensitive to H2O2 treatment (Fig. 1) and show a decreased lifespan during chronological ageing (Fig. 2A), which coincided with the appearance of apoptotic markers (Fig. 2B-D). A role for Bre1p in yeast cell death has not been assumed, but is consistent with the recent identification of its C. elegans homologue as a regulator of germ-cell apoptosis in worms (Lettre et al., 2004). Therefore, the anti-apoptotic function of Bre1p is probably evolutionary conserved and it will be interesting to see whether, for example, the human homologues of Bre1p, RNF20 and RNF40, are also implicated in apoptosis regulation.

The ability of Bre1p to reduce cell death is conferred by its E3 ubiquitin ligase activity and histone H2B ubiquitylation (Figs 3 and 4). Bre1p harbours a C-terminal zinc-binding motif known as the RING-finger domain (Hwang et al., 2003) that is frequently found in E3 ubiquitin ligases and is required for catalysing the transfer of ubiquitin from the E2 to the substrate (Deshaies and Joazeiro, 2009). RING domains appear to be crucial for apoptosis regulation, because members of the inhibitor-of-apoptosis protein (IAP) family comprise RING domains, which enable IAPs to mark other proteins such as caspases for proteasomal degradation (Wilson et al., 2002). Our data indicate that, in addition to polyubiquitylation, monoubiquitylation might have a role in apoptosis. We show that Δbre1 cells complemented with the RING-finger mutants ProtA-Bre1p(C648G, C651G) and ProtA-
Bre1p(L650E) lack monoubiquitylated histone H2B (Fig. 3A) and exhibit increased apoptosis sensitivity similarly to Δbre1 cells, whereas Δbre1 cells complemented with a functional ProtA-Bre1p behave in a similar manner to wild-type cells (Fig. 3). These findings suggest that Bre1p requires its E3 ligase activity to confer H2B monoubiquitylation and apoptosis resistance and support the notion that RING domains have a major role in apoptosis regulation.

The importance of H2B monoubiquitylation for the anti-apoptotic activity of Bre1p is further supported by our observation that hhi1-K123R mutant cells, which fail to ubiquitylate histone H2B, also exhibit increased apoptosis sensitivity, similarly to Δbre1 cells (Fig. 4A,B). Interestingly, yeast cells that exhibit enhanced levels of ubiquitylated histone H2B owing to the lack of the ubiquitin-specific protease Ubp10p, which cleaves the ubiquitin moiety from histone H2B, are also prone to apoptosis (Bettiga et al., 2004; Emre et al., 2005; Gardner et al., 2005). These data indicate that high levels of histone H2B ubiquitylation can also predispose yeast to apoptotic stimuli in a similar manner to the lack of histone H2B ubiquitylation. However, this study did not address whether or not Δubp10 cells show increased caspase activity due to high ubiquitylation levels of histone H2B. It is therefore possible that Ubp10p has other targets than ubiquitylated H2B and failure in deubiquitylation of these targets might cause sensitivity to apoptosis in these cells. To rule out this possibility, we analysed the apoptosis sensitivity of Δbre1 Δubp10. We expected that this double mutant would exhibit increased apoptosis sensitivity when compared with Δbre1 cells, if Ubp10p acted in a histone-H2B-independent manner. However, Δbre1 and Δbre1 Δubp10 cells showed similar apoptosis sensitivity during chronological ageing (supplementary material Fig. S4A). After 2 days in culture, BRE1-null cells showed survival rates of 23±4% compared with 24±2% in Δbre1 Δubp10 cells (supplementary material Fig. S4A). In addition, Δbre1 Δubp10 and Δbre1 cells showed similar survival rates after H2O2 treatment [31±5% cell viability versus 28±3% cell viability (supplementary material Fig. S4B)]. These data suggest that UBP10 disruption causes apoptosis sensitivity because of failures in histone H2B ubiquitylation. Therefore, the lack of histone H2B ubiquitylation, as well as high levels of histone H2B ubiquitylation, appear to predispose yeast to apoptotic stimuli, indicating that H2B ubiquitylation needs to be tightly regulated to ensure cell survival.

The yeast metacaspase Yca1p appears to be essential for approximately 40% of the investigated cell-death scenarios in yeast (Madeo et al., 2009) and we show here that apoptosis in Δbre1 cells in fact depends on Yca1p, because YCA1 disruption leads to reduced apoptosis sensitivity in cells lacking Bre1p (Fig. 5). Furthermore, the death of Δbre1 cells depends neither on other pro-apoptotic factors, such as EndoG, Nma111p nor on Aif1p (supplementary material Fig. S2), indicating that Bre1p anti-apoptotic activity is, at least in part, caspase dependent. Consistently, we show that Δbre1 cells exhibit increased caspase activity compared with wild-type cells (Fig. 6), suggesting that the caspase-like activity of Yca1p is implicated in the death of Δbre1 cells.

Possible mechanisms

Our data suggest that lack of histone H2B monoubiquitylation leads to Yca1p-dependent apoptosis during chronological ageing and after H2O2 treatment. Histone H2B ubiquitylation has a role in the DNA-damage response, as well as in transcriptional control (Briggs et al., 2001; Dover et al., 2002; Game et al., 2006; Giannattasio et al., 2005; Henry et al., 2003; Kao et al., 2004; Mutiu et al., 2007; Sun and Allis, 2002; Wyce et al., 2007; Xiao et al., 2005). Therefore, cells lacking histone H2B ubiquitylation might undergo Yca1p-dependent apoptosis, either because of accumulated DNA damage, or because of alterations in transcription. Although H2B ubiquitylation has been implicated in transcriptional silencing (Briggs et al., 2001; Mutiu et al., 2007; Sun and Allis, 2002), other studies suggested a positive role for this modification in transcriptional initiation and elongation (Henry et al., 2003; Kao et al., 2004; Wyce et al., 2007; Xiao et al., 2005). Notably, the core apoptotic machinery, including caspases and other regulators of apoptosis, are regulated at the transcriptional level in higher eukaryotes (Zuckerman et al., 2009). Therefore, it is possible that this balance is disturbed in cells lacking H2B ubiquitylation and up- or down-regulated transcription of apoptotic regulators causes apoptosis of these cells. It would be interesting to see whether YCA1 or other pro-apoptotic proteins are transcriptionally deregulated in Δbre1 cells. Furthermore, comparison of global mRNA transcripts between wild-type and Δbre1 cells could help to identify novel regulators of apoptosis.

Histone H2B ubiquitylation is required for Rad9p-mediated checkpoint activation after DNA damage and Rad51p-dependent DNA repair (Game et al., 2006; Giannattasio et al., 2005). Therefore, cells lacking histone H2B ubiquitylation might undergo Yca1p-dependent apoptosis because of accumulated DNA damage. However, neither Δrad9 nor Δrad51 cells exhibit apoptosis sensitivity similar to that observed in Δbre1 cells (our unpublished results), indicating that apoptosis in Δbre1 is not caused by defects in Rad9p or Rad51p pathways. Moreover, although Δbre1 cells exhibit sensitivity towards DNA damage induced by methyl methanesulfonate, hydroxyurea and UV radiation, respectively, disruption of Yca1p does not lead to a rescue in survival of Δbre1 cells under these conditions (data not shown). Therefore, we do not consider it likely that DNA damage causes Yca1p-dependent apoptosis in Δbre1 cells.

In conclusion, we show that Bre1p confers resistance to apoptosis and Yca1p is required in the apoptosis pathway triggered by BRE1 disruption. Bre1p is required for histone H2B ubiquitylation and its deletion, which influences transcriptional regulation and DNA repair, activates apoptosis. However, it remains to be seen whether transcription defects, failures in DNA repair, or both processes, activate the apoptotic program in cells lacking H2B ubiquitylation. Future studies in yeast will provide more details on the connection between transcription, DNA repair and apoptosis.

Materials and Methods

Plasmids, yeast strains and culture conditions

To construct the plasmid pBF326, which encodes ProtA-Bre1p, the coding region of BRE1 was amplified from genomic DNA isolated from BY4742 cells, using the following primers: 5‘-CAT GCC ATG AGA ATG GCC GAG CCT GCT A-3‘ and 5‘-GGC GGA TCC TTA CAA GTG CTC TGT CAA TAA ATC-3‘. The PCR product was digested with NcoI and BamHI and cloned into pNOPATA1 (Hellmuth et al., 1998). Plasmids pBF346 and pBF499 coding for ProtA-Bre1p(C648G,C651G) and ProtA-Bre1p(L650E), respectively, were constructed by site-directed polymerase chain reaction (PCR) mutagenesis using pBF326 as template according to the manufacturer’s instructions (Stratagene, QuickChange Site-Directed Mutagenesis Kit).

Yeast strains are listed in supplementary material Table S1. BY4742 (MATa; his3Δ1; leu2Δ0; lys2Δ0; ura3Δ0) and derivative strain Δbre1 were obtained from Euroscarf. Δubp10 strain was derived from BY4742 and constructed according to Longtine et al. (Longtine et al., 1998). The construction of Δbre1Δubp10, Δbre1 Δubp10 Δendog, Δbre1 Δubp10 Δnma111, Δbre1 Δubp10 Δaif1 and Δbre1 Δubp10 double-mutant strains was performed according to published methods (Gueddener et al., 2002). Yeast strains YIZS276 (FLAG-HB1) and YIZS277 (FLAG-hyb1K1238) were a gift from C. David Allis (Rockefeller University, New York, NY) (Sun and Allis, 2002a).
Δbre1 FLAG-HTB1 and Δbre1 FLAG-htb1K1238 were derived from YZS276 and YZS277, respectively, and constructed as described previously (Wolfgang and Madura, 1996). Apoptotic phosphorylation of histone H2B is mediated by mammalian sterile twenty kinase. Cell 113, 507-517.


<table>
<thead>
<tr>
<th>Yeast strain</th>
<th>Genotype</th>
<th>Source</th>
</tr>
</thead>
<tbody>
<tr>
<td>BY4742</td>
<td>MAT_ his3 1, leu2 0, lys2 0, ura3 0</td>
<td>Euroscarf</td>
</tr>
<tr>
<td>BFY177</td>
<td>MAT_ his3 1, leu2 0, lys2 0, ura3 0, YDL074c::kanMX4</td>
<td>Euroscarf</td>
</tr>
<tr>
<td>BFY324</td>
<td>MAT_ his3 1, leu2 0, lys2 0, ura3 0, YDL074c::LEU, YOR197W::kanMX4</td>
<td>This study</td>
</tr>
<tr>
<td>BFY402</td>
<td>MAT_ his3 1, leu2 0, lys2 0, ura3 0, YJL208C::kanMX4, YDL074c::LEU</td>
<td>This study</td>
</tr>
<tr>
<td>BFY323</td>
<td>MAT_ his3 1, leu2 0, lys2 0, ura3 0, YNL123W::kanMX4, YDL074c::LEU</td>
<td>This study</td>
</tr>
<tr>
<td>BFY403</td>
<td>MAT_ his3 1, leu2 0, lys2 0, ura3 0, YNR074C::kanMX4, YDL074c::LEU</td>
<td>This study</td>
</tr>
<tr>
<td>YZS276</td>
<td>MATa, ura3 1, trp1 1, leu2 3, his3 11, ade2 1, can1 100, hta1-htb1::LEU2 hta2-htb2 &lt;pZS145 HTA1-Flag-HTB1, CEN, HIS3&gt;</td>
<td>(Sun and Allis, 2002a)</td>
</tr>
<tr>
<td>YZS277</td>
<td>MATa, ura3 1, trp1 1, leu2 3, his3 11, ade2 1, can1 100, hta1-htb1::LEU2 hta2-htb2 &lt;pZS146 HTA1-Flag-htb1-K123R, CEN, HIS3&gt;</td>
<td>(Sun and Allis, 2002a)</td>
</tr>
<tr>
<td>BFY508</td>
<td>MATa, ura3 1, trp1 1, leu2 3, his3 11, ade2 1, can1 100, hta1-htb1::LEU2 hta2-htb2, YDL074c::kanMX4 &lt;pZS146 HTA1-Flag-htb1-K123R, CEN, HIS3&gt;</td>
<td>This study</td>
</tr>
<tr>
<td>BFY507</td>
<td>MATa, ura3 1, trp1 1, leu2 3, his3 11, ade2 1, can1 100, hta1-htb1::LEU2 hta2-htb2, YDL074c::kanMX4 &lt;pZS146 HTA1-Flag-htb1-K123R, CEN, HIS3&gt;</td>
<td>This study</td>
</tr>
<tr>
<td>BFY191</td>
<td>MAT_ his3 1, leu2 0, lys2 0, ura3 0:YDL074c::kanMX4, YDR224C::YDR224C-GFP-HIS3-MX6 &lt;PBF316 pNOPPATAI-BRE1&gt;</td>
<td>This study</td>
</tr>
<tr>
<td>BFY190</td>
<td>MAT_ his3 1, leu2 0, lys2 0, ura3 0, YDL074c::kanMX4 &lt;PBF316</td>
<td>This study</td>
</tr>
<tr>
<td>Strain</td>
<td>Genotype</td>
<td>Description</td>
</tr>
<tr>
<td>--------</td>
<td>----------</td>
<td>-------------</td>
</tr>
<tr>
<td>BFY192</td>
<td>MAT(_\alpha) his3 1, leu2 0, lys2 0, ura3 0, YDL074c::kanMX4 &lt;PBF346 pNOPPATAIL-bre1C648G,C651G&gt;</td>
<td>This study</td>
</tr>
<tr>
<td>BFY512</td>
<td>MAT(_\alpha) his3 1, leu2 0, lys2 0, ura3 0, YDL074c::kanMX4 &lt; pBF499 pNOPPATAIL-bre1L650E&gt;</td>
<td>This study</td>
</tr>
<tr>
<td>BFY193</td>
<td>MAT(_\alpha) his3 1, leu2 0, lys2 0, ura3 0, YDL074c::kanMX4, YDR224C::YDR224C-GFP-HIS3-MX6 &lt; PBF346 pNOPPATAIL-bre1C648G,C651G&gt;</td>
<td>This study</td>
</tr>
<tr>
<td>BFY510</td>
<td>MAT(_\alpha) his3 1, leu2 0, lys2 0, ura3 0, YDL074c::kanMX4, YDR224C::YDR224C-GFP-HIS3-MX6 &lt; pBF499 pNOPPATAIL-bre1L650E&gt;</td>
<td>This study</td>
</tr>
<tr>
<td>BFY199</td>
<td>MAT(_\alpha) his3 1, leu2 0, lys2 0, ura3 0 &lt;PBF316 pNOPPATAIL-BRE1&gt;</td>
<td>This study</td>
</tr>
<tr>
<td>BFY200</td>
<td>MAT(_\alpha) his3 1, leu2 0, lys2 0, ura3 0, YDL074c::kanMX4 &lt;PBF005 pNOPPATAIL&gt;</td>
<td>This study</td>
</tr>
<tr>
<td>BFY201</td>
<td>MAT(_\alpha) his3 1, leu2 0, lys2 0, ura3 0&lt; PBF005 pNOPPATAIL&gt;</td>
<td>This study</td>
</tr>
<tr>
<td>BFY514</td>
<td>MAT(_\alpha) his3 1, leu2 0, lys2 0, ura3 0, YNL186W::LEU</td>
<td>This study</td>
</tr>
<tr>
<td>BFY515</td>
<td>MAT(_\alpha) his3 1, leu2 0, lys2 0, ura3 0, YDL074c::kanMX4, YNL186W::LEU</td>
<td>This study</td>
</tr>
</tbody>
</table>